SEQUENCE LISTING

<110>   BASF Plant Science GmbH

<120>   Expression of Phospholipids:Diacylglycerine Acyltransferase (PDAT) for
the Production of Plant Storage Lipids with Polyunsaturated Fatty Acids

<130>   1
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<170>   PatentIn version 3.1
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<211>   2425
<212>   DNA
<213>   Physcomitrella patens

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<221>   CDS

<222>   (120)..(2135)

<223>   Phospholipid:Diacylglycerin-Acyltransferase


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atg ccc ctt att cat cgg aaa aag ccg acg gag aaa cca tcg acg ccg         167
Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro
1               5                   10                  15

cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac         215
Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His
            20                  25                  30

gaa tct tcc aaa tcc cac cat aag aaa tcg aac gga gga ggg aag tgg         263
Glu Ser Ser Lys Ser His His Lys Lys Ser Asn Gly Gly Gly Lys Trp
        35                  40                  45

tcg tgc atc gat tct tgt tgt tgg ttc att ggg tgt gtg tgt gta acc         311
Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
    50                  55                  60

tgg tgg ttt ctt ctc ttc ctt tac aac gca atg cct gcg agc ttc cct         359
Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
65                  70                  75                  80

cag tat gta acg gag cga atc acg ggt cct ttg cct gac ccg ccc ggt         407
Gln Tyr Val Thr Glu Arg Ile Thr Gly Pro Leu Pro Asp Pro Pro Gly
                85                  90                  95

gtt aag ctc aaa aaa gaa ggt ctt aag gcg aaa cat cct gtt gtc ttc         455
Val Lys Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe

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att cct ggg att gtc acc ggt ggg ctc gag ctt tgg gaa ggc aaa caa    503
Ile Pro Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln
        115             120             125

tgc gct gat ggt tta ttt aga aaa cgt ttg tgg ggt gga act ttt ggt    551
Cys Ala Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Gly
        130             135             140

gaa gtc tac aaa agg cct cta tgt tgg gtg gaa cac atg tca ctt gac    599
Glu Val Tyr Lys Arg Pro Leu Cys Trp Val Glu His Met Ser Leu Asp
145             150             155             160

aat gaa act ggg ttg gat cca gct ggt att aga gtt cga gct gta tca    647
Asn Glu Thr Gly Leu Asp Pro Ala Gly Ile Arg Val Arg Ala Val Ser
            165             170             175

gga ctc gtg gct gct gac tac ttt gct cct ggc tac ttt gtc tgg gca    695
Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala
            180             185             190

gtg ctg att gct aac ctt gca cat att gga tat gaa gag aaa aat atg    743
Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met
            195             200             205

tac atg gct gca tat gac tgg cgg ctt tcg ttt cag aac aca gag gta    791
Tyr Met Ala Ala Tyr Asp Trp Arg Leu Ser Phe Gln Asn Thr Glu Val
    210             215             220

cgt gat cag act ctt agc cgt atg aaa agt aat ata gag ttg atg gtt    839
Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val
225             230             235             240

tct acc aac ggt gga aaa aaa gca gtt ata gtt ccg cat tcc atg ggg    887
Ser Thr Asn Gly Gly Lys Lys Ala Val Ile Val Pro His Ser Met Gly
            245             250             255

gtc ttg tat ttt cta cat ttt atg aag tgg gtt gag gca cca gct cct    935
Val Leu Tyr Phe Leu His Phe Met Lys Trp Val Glu Ala Pro Ala Pro
            260             265             270

ctg ggt ggc ggg ggt ggg cca gat tgg tgt gca aag tat att aag gcg    983
Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala
            275             280             285

gtg atg aac att ggt gga cca ttt ctt ggt gtt cca aaa gct gtt gca   1031
Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala
            290             295             300

ggg ctt ttc tct gct gaa gca aag gat gtt gca gtt gcc aga gcg att   1079
Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile
305             310             315             320

gcc cca gga ttc tta gac acc gat ata ttt aga ctt cag acc ttg cag   1127
Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln
            325             330             335
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cat gta atg aga atg aca cgc aca tgg gac tca aca atg tct atg tta      1175
His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu
            340                 345                 350

ccg aag gga ggt gac acg ata tgg ggc ggg ctt gat tgg tca ccg gag      1223
Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu
            355                 360                 365

aaa ggc cac acc tgt tgt ggg aaa aag caa aag aac aac gaa act tgt      ·1271
Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys
     370                 375                 380

ggt gaa gca ggt gaa aac gga gtt tcc aag aaa agt cct gtt aac tat      1319
Gly Glu Ala Gly Glu Asn Gly Val Ser Lys Lys Ser Pro Val Asn Tyr
385                 390                 395                 400

gga agg atg ata tct ttt ggg aaa gaa gta gca gag gct gcg cca tct      1367
Gly Arg Met Ile Ser Phe Gly Lys Glu Val Ala Glu Ala Ala Pro Ser
                405                 410                 415

gag att aat aat att gat ttt cga ggt gct gtc aaa ggt cag agt atc      ·1415
Glu Ile Asn Asn Ile Asp Phe Arg Gly Ala Val Lys Gly Gln Ser Ile
            420                 425                 430

cca aat cac acc tgt cgt gac gtg tgg aca gag tac cat gac atg gga      1463
Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly
            435                 440                 445

att gct ggg atc aaa gct atc gct gag tat aag gtc tac act gct ggt      1511
Ile Ala Gly Ile Lys Ala Ile Ala Glu Tyr Lys Val Tyr Thr Ala Gly
     450                 455                 460

gaa gct ata gat cta cta cat tat gtt gct cct aag atg atg gcg cgt      1559
Glu Ala Ile Asp Leu Leu His Tyr Val Ala Pro Lys Met Met Ala Arg
465                 470                 475                 480

ggt gcc gct cat ttc tct tat gga att gct gat gat ttg gat gac acc      ·1607
Gly Ala Ala His Phe Ser Tyr Gly Ile Ala Asp Asp Leu Asp Asp Thr
                485                 490                 495

aag tat caa gat ccc aaa tac tgg tca aat ccg tta gag aca aaa tta      1655
Lys Tyr Gln Asp Pro Lys Tyr Trp Ser Asn Pro Leu Glu Thr Lys Leu
            500                 505                 510

ccg aat gct cct gag atg gaa atc tac tca tta tac gga gtg ggg ata      1703
Pro Asn Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile
            515                 520                 525

cca acg gaa cga gca tac gta tac aag ctt aac cag tct ccc gac agt      1751
Pro Thr Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser
            530                 535                 540

tgc atc ccc ttt cag ata ttc act tct gct cac gag gag gac gaa gat      1799
Cys Ile Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp
545                 550                 555                 560
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agc tgt ctg aaa gca gga gtt tac aat gtg gat ggg gat gaa aca gta      1847
Ser Cys Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val
                565                 570                 575

ccc gtc cta agt gcc ggg tac atg tgt gca aaa gcg tgg cgt ggc aag      1895
Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys
                580                 585                 590

aca aga ttc aac cct tcc gga atc aag act tat ata aga gaa tac aat      1943
Thr Arg Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn
            595                 600                 605

cac tct ccg ccg gct aac ctg ttg gaa ggg cgc ggg acg cag agt ggt      1991
His Ser Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly
        610                 615                 620

gcc cat gtt gat atc atg gga aac ttt gct ttg atc gaa gat atc atg      2039
Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met
625                 630                 635                 640

agg gtt gcc gcc gga ggt aac ggg tct gat ata gga cat gac cag gtc      2087
Arg Val Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val
                645                 650                 655

cac tct ggc ata ttt gaa tgg tcg gag cgt att gac ctg aag ctg tga      2135
His Ser Gly Ile Phe Glu Trp Ser Glu Arg Ile Asp Leu Lys Leu
                660                 665                 670

atatcatgat ctctttaagc tgtcctgtca gcttatgtga atccaatact ttgaaagaga     2195

gatcatcatc aattcatcat catcgtcatc atcatgatgc tcaactcaca aagaagcctg     2255

agaatgatac tttggtgcga aattctcaat acctctttaa tattcttatt gaatgtaaat     2315

tatacaatcc tatctaatgt ttgaacgata acacaaaact tgctgcgcca tgtttgtttg     2375

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<212>  PRT

<213>  Physcomitrella patens


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Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro
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Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His
            20                  25                  30

Glu Ser Ser Lys Ser His His Lys Lys Ser Asn Gly Gly Gly Lys Trp
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              35                    40                    45

Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
    50              55              60

Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
65              70              75              80

Gln Tyr Val Thr Glu Arg Ile Thr Gly Pro Leu Pro Asp Pro Pro Gly
            85              90              95

Val Lys Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe
            100             105             110

Ile Pro Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln
        115             120             125

Cys Ala Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Gly
    130             135             140

Glu Val Tyr Lys Arg Pro Leu Cys Trp Val Glu His Met Ser Leu Asp
145             150             155             160

Asn Glu Thr Gly Leu Asp Pro Ala Gly Ile Arg Val Arg Ala Val Ser
            165             170             175

Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala
        180             185             190

Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met
    195             200             205

Tyr Met Ala Ala Tyr Asp Trp Arg Leu Ser Phe Gln Asn Thr Glu Val
    210             215             220

Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val
225             230             235             240

Ser Thr Asn Gly Gly Lys Lys Ala Val Ile Val Pro His Ser Met Gly
            245             250             255

Val Leu Tyr Phe Leu His Phe Met Lys Trp Val Glu Ala Pro Ala Pro
        260             265             270

Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala
    275             280             285

Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala
    290             295             300

Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile
305             310             315             320

Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln
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                325                    330                    335

His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu
            340                    345                    350

Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu
            355                    360                    365

Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys
    370                    375                    380

Gly Glu Ala Gly Glu Asn Gly Val Ser Lys Lys Ser Pro Val Asn Tyr
385                    390                    395                    400

Gly Arg Met Ile Ser Phe Gly Lys Glu Val Ala Glu Ala Ala Pro Ser
                405                    410                    415

Glu Ile Asn Asn Ile Asp Phe Arg Gly Ala Val Lys Gly Gln Ser Ile
            420                    425                    430

Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly
            435                    440                    445

Ile Ala Gly Ile Lys Ala Ile Ala Glu Tyr Lys Val Tyr Thr Ala Gly
    450                    455                    460

Glu Ala Ile Asp Leu Leu His Tyr Val Ala Pro Lys Met Met Ala Arg
465                    470                    475                    480

Gly Ala Ala His Phe Ser Tyr Gly Ile Ala Asp Asp Leu Asp Asp Thr
                485                    490                    495

Lys Tyr Gln Asp Pro Lys Tyr Trp Ser Asn Pro Leu Glu Thr Lys Leu
            500                    505                    510

Pro Asn Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile
            515                    520                    525

Pro Thr Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser
    530                    535                    540

Cys Ile Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp
545                    550                    555                    560

Ser Cys Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val
                565                    570                    575

Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys
            580                    585                    590

Thr Arg Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn
            595                    600                    605

His Ser Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly
    610                    615                    620

Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met
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625                   630                   635                   640

Arg Val Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val
                 645             650                 655

His Ser Gly Ile Phe Glu Trp Ser Glu Arg Ile Asp Leu Lys Leu
             660             665                 670
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